

#28

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/057,843C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos  
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length  
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering  
The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII  
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length  
Sequence(s)          contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)         . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)  
Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)  
Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9      Use of n's or Xaa's  
    (NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response  
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>  
Sequence(s) 1-2 (maybe more) missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"  
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n  
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

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1600

## RAW SEQUENCE LISTING

DATE: 05/29/2002

PATENT APPLICATION: US/09/051,843C

TIME: 16:33:26

Input Set : A:\11373.txt

Output Set: N:\CRF3\05292002\I051843C.raw

*pp 1316*  
**Does Not Comply**  
**Corrected Diskette Needed**

3 <110> APPLICANT: Willson, Tracy  
 4 Nicola, Nicos A.  
 5 Hilton, Douglas J.  
 6 Metcalf, Donald  
 7 Zhang, Jian G.  
 9 <120> TITLE OF INVENTION: NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES  
 10 ENCODING SAME  
 12 <130> FILE REFERENCE: Davies cc  
 14 <140> CURRENT APPLICATION NUMBER: 09/051,843C  
 15 <141> CURRENT FILING DATE: 1998-06-29  
 17 <160> NUMBER OF SEQ ID NOS: 11  
 19 <170> SOFTWARE: PatentIn Ver. 2.0  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 1383  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Unknown *see item 11 on Env Summary Sheet*  
 26 <220> FEATURE:  
 27 <221> NAME/KEY: CDS  
 28 <222> LOCATION: (61)..(1338)  
 30 <220> FEATURE:  
 31 <221> NAME/KEY: unsure  
 32 <222> LOCATION: (121)  
 33 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this  
 34 region  
 36 <220> FEATURE:  
 37 <221> NAME/KEY: unsure  
 38 <222> LOCATION: (122)  
 39 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this  
 40 region  
 42 <220> FEATURE:  
 43 <221> NAME/KEY: unsure  
 44 <222> LOCATION: (123)  
 45 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this  
 46 region  
 48 <220> FEATURE:  
 49 <221> NAME/KEY: unsure  
 50 <222> LOCATION: (640)  
 51 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this  
 52 region  
 55 <220> FEATURE:  
 56 <221> NAME/KEY: unsure  
 57 <222> LOCATION: (641)  
 58 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this

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59      region
61 <220> FEATURE:
62 <221> NAME/KEY: unsure
63 <222> LOCATION: (642)
64 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
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67 <400> SEQUENCE: 1
68 tgaaaagata gaataaatgg cctcgtgccg aattcggcac gagccgaggc gagggcctgc 60
70 atg gcg cgg cca gcg ctg ctg ggc gag ctg ttg gtg ctg cta ctg tgg 108
71 Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp
72 1 5 10 15
74 acc gcc acc gtg nnn ggc caa gtt gcc gcg gcc aca gaa gtt cag cca 156
75 Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro
76 20 25 30
78 cct gtg acg aat ttg agc gtc tct gtc gaa aat ctc tgc acg ata ata 204
79 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile
80 35 40 45
82 tgg acg tgg agt cct cct gaa gga gcc agt cca aat tgc act ctc aga 252
83 Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
84 50 55 60
86 tat ttt agt cac ttt gat gac caa cag gat aag aaa att gct cca gaa 300
87 Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
88 65 70 75 80
90 act cat cgt aaa gag gaa tta ccc ctg gat gag aaa atc tgt ctg cag 348
91 Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
92 85 90 95
94 gtg ggc tct cag tgt agt gcc aat gaa agt gag aag cct agc cct ttg 396
95 Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
96 100 105 110
98 gtg aaa aag tgc atc tca ccc cct gaa ggt gat cct gag tcc gct gtg 444
99 Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
100 115 120 125
102 act gag ctc aag tgc att tgg cat aac ctg agc tat atg aag tgt tcc 492
103 Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
104 130 135 140
106 tgg ctc cct gga agg aat aca agc cct gac aca cac tat act ctg tac 540
107 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr
108 145 150 155 160
110 tat tgg tac agc agc ctg gag aaa agt cgt caa tgt gaa aac atc tat 588
111 Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr
112 165 170 175
114 aga gaa ggt caa cac att gct tgt tcc ttt aaa ttg act aaa gtg gaa 636
115 Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu
116 180 185 190
118 cct nnn agt ttt gaa cat cag aac gtt caa ata atg gtc aag gat aat 684
119 Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn
120 195 200 205
122 gct ggg aaa att agg cca tcc tgc aaa ata gtg tct tta act tcc tat 732
123 Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr

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124      210      215      220
126 gtg aaa cct gat cct cca cat att aaa cat ctt ctc ctc aaa aat ggt 780
127 Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly
128 225      230      235      240
130 gcc tta tta gtg cag tgg aag aat cca caa aat ttt aga agc aga tgc 828
131 Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys
132      245      250      255
134 tta act tat gaa gtg gag gtc aat aat act caa acc gac cga cat aat 876
135 Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn
136      260      265      270
138 att tta gag gtt gaa gag gac aaa tgc cag aat tcc gaa tct gat aga 924
139 Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg
140      275      280      285
142 aac atg gag ggt aca agt tgt ttc caa ctc cct ggt gtt ctt gcc gac 972
143 Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp
144      290      295      300
146 gct gtc tac aca gtc aga gta aga gtc aaa aca aag tta tgc ttt 1020
147 Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe
148 305      310      315      320
150 gat gac aac aaa ctg tgg agt gat tgg agt gaa gca cag agt ata ggt 1068
151 Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly
152      325      330      335
154 aag gag caa aac tcc acc ttc tac acc acc atg tta ctc acc att cca 1116
155 Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro
156      340      345      350
158 gtc ttt gtc gca gtg gca gtc ata atc ctc ctt ttt tac ctg aaa agg 1164
159 Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
160      355      360      365
162 ctt aag atc att ata ttt cct cca att cct gat cct ggc aag att ttt 1212
163 Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
164      370      375      380
166 aaa gaa atg ttt gga gac cag aat gat gat acc ctg cac tgg aag aag 1260
167 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
168 385      390      395      400
170 tat gac atc tat gag aaa caa tcc aaa gaa gaa acg gat tct gta gtg 1308
171 Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
172      405      410      415
174 ctg ata gaa aac ctg aag aaa gca gct cct tgatggggag aagtgatttc 1358
175 Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro
176      420      425
178 tttcttgcc tcaatgtgac cctgt 1383
181 <210> SEQ ID NO: 2
182 <211> LENGTH: 426
183 <212> TYPE: PRT
184 <213> ORGANISM: Unknown
186 <220> FEATURE:
187 <221> NAME/KEY: unsure
188 <222> LOCATION: (21)
189 <223> OTHER INFORMATION: authors are unsure about the sequence assignment

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*see item 11*

*Please correct any subsequent sequences showing this error.*

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191 &lt;220&gt; FEATURE:

193 &lt;221&gt; NAME/KEY: unsure

194 &lt;222&gt; LOCATION: (194)

195 &lt;223&gt; OTHER INFORMATION: authors are unsure about the sequence assignment

197 &lt;400&gt; SEQUENCE: 2

198 Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp

199 1 5 10 15

W-201 Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro

202 20 25 30

204 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile

205 35 40 45

207 Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg

208 50 55 60

210 Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu

211 65 70 75 80

213 Thr His Arg Lys Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln

214 85 90 95

216 Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu

217 100 105 110

219 Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val

220 115 120 125

222 Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser

223 130 135 140

225 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr

226 145 150 155 160

228 Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr

229 165 170 175

231 Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu

232 180 185 190

W-234 Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn

235 195 200 205

237 Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr

238 210 215 220

240 Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Lys Asn Gly

241 225 230 235 240

243 Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys

244 245 250 255

246 Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn

247 260 265 270

249 Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg

250 275 280 285

252 Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp

253 290 295 300

255 Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe

256 305 310 315 320

258 Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly

259 325 330 335

262 Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro

263 340 345 350

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265 Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
266          355          360          365
268 Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
269          370          375          380
271 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
272 385          390          395          400
274 Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
275          405          410          415
277 Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro
278          420          425
281 <210> SEQ ID NO: 3
282 <211> LENGTH: 1383
283 <212> TYPE: DNA
284 <213> ORGANISM: Homo sapiens
286 <220> FEATURE:
287 <221> NAME/KEY: CDS
288 <222> LOCATION: (61)..(1338)
290 <400> SEQUENCE: 3
291 gagtctaaca cggaccaagg agtttaacac gtgcggccgg gttccgaggg gagaggctgc 60
293 atg gag tgg ccg gcg cgg ctc tgc ggg ctg tgg gcg ctg ctg ctc tgc 108
294 Met Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Leu Cys
295 1          5          10          15
297 gcc gcc gcc ggg gcc ggg gcc ggg gcc ggc cct acg gaa act cag cca 156
298 Ala Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Thr Glu Thr Gln Pro
299          20          25          30
301 cct gtg aca aat ttg agt gtc tct gtt gaa aac ctc tgc aca gta ata 204
302 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile
303          35          40          45
305 tgg aca tgg aat cca ccc gag gga gcc agc tca aat tgt agt cta tgg 252
306 Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp
307          50          55          60
309 tat ttt agt cat ttt ggc gac aaa caa gat aag aaa ata gct ccg gaa 300
310 Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu
311 65          70          75          80
313 act cgt cgt tca ata gaa gta ccc ctg aat gag agg att tgt ctg .caa 348
314 Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln
315          85          90          95
317 gtg ggg tcc cag tgt agc acc aat gag agt gag aag cct agc att ttg 396
318 Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu
319          100          105          110
321 gtt gaa aaa tgc atc tca ccc cca gaa ggt gat cct gag tct gct gtg 444
322 Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
323          115          120          125
325 act gag ctt caa tgc att tgg cac aac ctg agc tac atg aag tgt tct 492
326 Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
327          130          135          140
329 tgg ctc cct gga agg aat acc agt ccc gac act aac tat act ctc tac 540
330 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr
331 145          150          155          160

```

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Input Set : A:\11373.txt  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 121,122,123,640,641,642

Seq#:1; Xaa Pos. 21,194

Seq#:2; Xaa Pos. 21,194

Seq#:9; Xaa Pos. 3

Seq#:10; Xaa Pos. 24

Seq#:11; Xaa Pos. 24